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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/937,779	07/02/2002	Anders Dahlqvist	0093/000003	7114
26474	7590	05/09/2006		EXAMINER
				ROBINSON, HOPE A
			ART UNIT	PAPER NUMBER
				1656

DATE MAILED: 05/09/2006

Please find below and/or attached an Office communication concerning this application or proceeding.



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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT PAPER

050406

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

The sequence listing filed on November 18, 2005 does not comply with the sequence rules see the attached error report and notice to comply.

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825; applicant's attention is directed to the final rule making notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). To be in compliance, applicant is required to identify all amino acid sequences of at least 4 L-amino acids and at least 10 nucleotides by a sequence identifier, i.e., "SEQ ID NO:". The sequence listing provided has errors therefore, applicant must provide a computer readable form of the "Sequence Listing" including these sequences, a paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification, and a statement that the content of the paper and computer readable form copies are the same and, where applicable, include no new matter as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.821(b) or 1.825(d). See the attached Notice to Comply with the sequence rules.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Hope A. Robinson whose telephone number is 571-272-0957. The examiner can normally be reached on Monday-Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Kathleen Kerr, can be reached at (571) 272-0931. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Hope Robinson, MS
Patent Examiner

5/11/06
HOPE A. ROBINSON
PATENT EXAMINER

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
7. Other: See Raw Sequence Listing Error Report

8. Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216 or (703) 308-2923
- For CRF Submission Help, call (703) 308-4212
- For PatentIn software Program Support:
 - HELP DESK: (703) 739-8559, ext 508, M-F, 8 AM to 5 PM EST except holidays
 - Email: PATIN21HELP@uspto.gov
 - To purchase PatentIn software: (703) 306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/937,779 A

Source: TFLW16

Date Processed by STIC: 11/18/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/937,779 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

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Output Set: N:\CRF4\11182005\I937779A.raw

3 <110> APPLICANT: Dahlqvist, Anders
4 Stahl, Ulf
5 Lenman, Marit
6 Banas, Antoni
7 Ronne, Hans
8 Stymne, Sten

Does Not Comply
Damaged Diskette Needed
(pg - 1-17)

10 <120> TITLE OF INVENTION: PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES THAT
ENCODE

11 PHOSPHOLIPID: DIACYLGLYCEROL ACYLTRANSFERASES
13 <130> FILE REFERENCE: BASFnae337799PCT1-15
15 <140> CURRENT APPLICATION NUMBER: US 09/937779A
C--> 17 <141> CURRENT FILING DATE: 2002-07-02
17 <150> PRIOR APPLICATION NUMBER: PCT / EP 00 / 02701
18 <151> PRIOR FILING DATE: 2000-03-23
20 <160> NUMBER OF SEQ ID NOS: 32
22 <170> SOFTWARE: PatentIn Ver. 3.3

ERRORED SEQUENCES

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336 <211> LENGTH: 2312
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338 <213> ORGANISM: Schizosaccharomyces pombe
340 <400> SEQUENCE: 3

Invalid <212> Response
Per 1-823 of Seq Rules
Use "DNA" as response
and explain any modification
in <220-2237
Section.

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

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Output Set: N:\CRF4\11182005\I937779A.raw

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> same error

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

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Output Set: N:\CRP4\11182005\I937779A.raw

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Some type of error as
previous pages See page-4

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455 100 SEQUENCE 5

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463 tgtgtgtaaac ctggtggtttt cttctttcc tttacaacgc aatgcctgcg agcttcctc 360

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

Input Set : N:\RJAVER\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

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Output Set: N:\CRF4\11182005\I937779A.raw

655 tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg	144
656 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val	
657 35 40 45	
659 aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc	192
660 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly	
661 50 55 60	
663 acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att	240
664 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile	
665 65 70 75 80	
667 gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt	288
668 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly	
669 85 90 95	
671 ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa	336
672 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys	
673 100 105 110	
675 ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att	384
676 Leu Lys Leu	
677 115	
679 gcg ttc caa agt gtc ctg cctgagtgc actctggatt ttgcttaat	432
681 attgttaattt ttcacgttcc attcgtccct ttgtcaaatt tacatttgac aggacccaa	492
683 tgcgatacga tggtagtaccg ctatttcag cattgtatat taaaactgtac aggtgtaaat	552
W--> 685 tgcatttgcg agctgaaatt ttgttagtctgt ttctttacg atttaatanc aagtggcgga	612
W--> 687 gcagtgcggc aaggaaaaaaa aaaaaaaaaa a	643
716 <210> SEQ ID NO: 9	
717 <211> LENGTH: 616	
E--> 718 <212> TYPE: CDNA	Same Error
719 <213> ORGANISM: Neurospora crassa	See page 17
721 <400> SEQUENCE: 9	
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E--> 723 accctctaga gacacgacta cncntgcacc cagcctcaag gtntacngt tntatggta	120
724 ggaagccgac ggagcgggcc tacatctatc tggcgccccga tcccgggacg acaacgcac	180
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726 gcgaggcga tggcacatgt aaccttatga gtttgggta cctgtcaat aagggttgg	300
727 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcataaac	360
728 cagaacgggtt caatccgaga ggagggccga atacggcggta tcacgtggat atcttagaa	420
729 ggcagaatct aaacgagttac attcttaaag tggcggcagg tcgaggcgt acaatttgg	480
730 atttttattac tagtaatatt cttaaatatg tagaaaagg tggaaatttat gaagagtaat	540
731 taaatacggc acataggta ctcaatagta tgactaatta aaaaaaaaaatt tttttctaa	600
732 aaaaaaaaaa aaaaaaa	616
735 <210> SEQ ID NO: 10	
736 <211> LENGTH: 1562	
E--> 737 <212> TYPE: genomic DNA	Same Error
738 <213> ORGANISM: Arabidopsis thaliana	
740 <400> SEQUENCE: 10	
741 atgaaaaaaaaa tatcttcaca ttattcggtt gtcatacgca tactcggtt ggtgacgt	60
742 acctcgatgt gtcaagctgt gggtagcaac gtgtaccctt tgattctggt tccagaaac	120
743 ggaggttaacc agctagaggt acggctggac agagaataca agccaagtag tgtctgggt	180
744 agcagctgtt tatatccgtat tcataagaag agtgggtggat ggtttaggct atggttcgat	240
745 gcagcagtgtt tattgtctcc cttcaccagg tgcttcagcg atcgaatgtt gtttactat	300

RAW SEQUENCE LISTING
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Output Set: N:\CRF4\11182005\I937779A.raw

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747	ggttcgacca	aatcaacttct	atacctcgac	cctcgctcc	ggtagtact	ttccaagata	420
748	tatcattttg	ggacatttc	ataatgaaca	aatagacat	aaatttgggg	gattattgtt	480
749	atataaatat	ccatttatat	gctagtccgt	aatgtgagtg	ttatgttagt	atagttaatg	540
750	tgaatgttat	gtgatttcc	attttaatg	aagctagaaa	gttgcgtt	aataatgtt	600
751	ctatgtcatg	agaattataa	ggacactatg	taaatgttagc	ttaataataa	ggtttgattt	660
752	gcagagatgc	cacatcttac	atggAACATT	tggtaaagc	tctagagaaa	aatgcgggt	720
753	atgttaaacga	ccaaaccatc	ctaggagctc	catatgattt	caggtacggc	ctggctgtt	780
754	cgggccaccc	gtcccggtt	gcctcacagt	tcctacaaga	cctcaaacaa	ttggtgaaaa	840
755	aaactagcag	cgagaacaa	ggaaAGCCAG	tgataactct	ctccccatagc	ctaggaggac	900
756	tttgcgtct	ccatttcctc	aaccgtacca	ccccttcatg	gchgcccaag	tacatcaaac	960
757	actttgtgc	actcgctcg	ccatgggtg	ggacgatctc	tcagatgaag	acatttgott	1020
758	ctggcaacac	actcggttc	ccttttagtt	accctttgt	ggtaagacgg	catcagagga	1080
759	cctccgagag	taaccaatgg	ctacttccat	ctaccaaaagt	gtttcacgac	agaactaaac	1140
760	cgttgtcgt	aactccccag	gttaactaca	cagcttacga	gatggatcgg	tttttgcaag	1200
761	acattggatt	ctcacaagga	gttgtgcct	acaagacaag	agtgttgct	ttaacagagg	1260
762	agctgatgac	tccggagtg	ccagtcactt	gcatatatgg	gagaggagtt	gatacacccgg	1320
763	aggttttgc	gtatggaaaa	ggaggattcg	ataagcaacc	agagattaag	tatggagatg	1380
764	gagatgggac	ggtaatttgc	gctgagcttgc	cagcttggaa	agtcgatagc	ttgaacacccg	1440
765	tagagattga	tggagtttc	catacatcta	tacttaaaga	cgagatcgca	cttaaagaga	1500
766	ttatgaagca	gattcaattt	attaattatg	aattagccaa	tgttaatgcc	gtcaatgaat	1560
767	qa						1562

1562

same error

E--> 772 <212> TYPE: genomic DNA
773 <213> ORGANISM: *Arabidopsis thaliana*
775 <400> SEQUENCE: 11

776 atgggagcga attcgaaatc agtaacggct tccttcaccg tcatcgccgt ttttttcttg 60
777 attgcgggt gccgaactgc ggtggaggat gagaccgagt ttacggcga ctactcgaag 120
778 ctatcggtta taatcattcc gggatttgcg tcgacgcagc tacgagcggtg gtcgatcctt 180
779 gactgtccat acactccgtt ggacttcaat cgcgtcgacc tctgtatggct agacaccaact 240
780 aaggccgtg atcttcattt ctttcgtcc ttattctgtc ggtcgagtca cttgtttagt 300
781 aattccaagc gaaatatagc aatgaagcat gtctcgctc tcttatttgcgat tcgttcat 360
782 gtcacagtg acgctctga atctgagttt agagtcataaaaacagctg actcggcgag 420
783 tggtttccat cgctttggt tegetaaatg tagcgeaatg aatgtgtat tagtctcgcc 480
784 tttttattca actagatctg caagttttc agagtgcata atagtagttt gaaaatgtta 540
785 ggtcatttta cttgtgcatt gtgattcttt tggttgttgc ttactgatcg acgtgatgga 600
786 tggtttacag cttcttctg ctgtcaactg ctggtttaag tgtatggtgc tagatccta 660
787 taatcaaaca gaccatcccc agtgtaagtc acggcctgac agtggctttt cagccatcac 720
788 agaatttggat ccaggttaca taacaggttag ttccggattt ttctttcttt tgagtttct 780
789 tcaatttgcgat atcatcttgc tgcgtatataa tatggctaaatg ttcatattt tggtcaattt 840
790 tcagggtcctc ttctactgt ctggaaagag tggcttaagt ggtgtgttgc gtttggata 900
791 gaagccaaatg caatttgcgc tggttccatac gattggagat tgcaccaac caaattggaa 960
792 gagcgtgacc ttactttca caagctcaag ttgcgttca tcaaggctaat gtcttttgc 1020
793 ttctctttt atgtaagata agctaagage tctgggtcgtc ttcccttttgc caggttgc 1080
794 ttggaaactg ctttaaaact ccgtggcgcc ccttcatacg tatttgccttcaatgggt 1140
795 aataatgtct tcagatactt tctggaaatgg ctgaggcttag aaattgcacc aaaacattat 1200
796 ttgaagtggc ttgatcgcata tattccatgt tatttcgttgc ttggtaaccgg cctactatcc 1260
797 ttaagttacc attttatccc ttctctaatt qqqqqqgtta ttttgcgtact tactqgattq 1320

RAW SEQUENCE LISTING DATE: 11/18/2005
PATENT APPLICATION: US/09/937,779A **TIME:** 10:08:48

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799 tcaaatctac tctctctgtt gtaacgttt gccttcctgt ttctgaggtg acctctgact 1440
800 tctcttagt ttaagttagt tgatatcaac caggctttat aactcactgg atttccctt 1500
801 tgaaggattt acttttgtt attgaactgc tgtaacgcat atggatctg tagatctga 1560
802 agtcttagt atcaaagaac atattgtggg tagtataacct gtcagcggcc ttagctaata 1620
803 caaccaaacc acatgtcac tggatgtttt ttcagattat tatggtagac ttaagttga 1680
804 gaagaaactt tgactgaaat ctttttattt taataggcta tgattgtttt attgaaatca 1740
805 tggacatata tggacatgcgc ttctcatgtt ttttgttggc aaggcttcag ggaactgctc 1800
806 ggttgggtc caattctttt gcgctgtcat tgggtttat gccattttca aagaattgca 1860
807 agggtgataa cacattctgg acgcattttt ctgggggtgc tgcaagaaaa gataagcgcg 1920
808 tataccactg tggatgaaag gaatatcaat caaaatattc tggctggccg acaaataattt 1980
809 ttaacattga aattccctcc actagcgggtt agactctgta tatgcaactg taacactaac 2040
810 aaaagtttca ccaagaatgt tcactctcat atttgcgtcc tttgatgtgt atccatca 2100
811 tacagaaaca gctctagtc acatgaccag catggaatgt ggccttccca ccctttgtc 2160
812 tttcacagcc cgtgaactag cagatgggac tttttcaaa gcaatagaag actatgaccc 2220
813 agatagcaag aggtatgttac accagttaaa gaagtacgtt ccttctttt tgataagaaaa 2280
814 tattgctcat cgatcatcac ttgtggctt ctgtacgtc aaattgtttt gtttaaatct 2340
815 ctatataat tggatcatatg ctttgtctt cttactataa gaaacaagta taatcagaaaa 2400
816 ccttattattt gattatcagt tctctctta tattatggaa tgtcttttc gtttacagtt 2460
817 atgaatgcaa aagggggtat ttttagttgt tgattctctc attctctagt ttgttttgac 2520
818 taatagcgtc aattttgttt ttctagcaaa tctttgtgaa ttatataaa catgctaact 2580
819 atactttca gggttatca tgatgaccct gttttaatc ctctgactcc ttggagaga 2640
820 ccacctataa aaaatgtatt ttgcataatat ggtgctcatc taaagacaga ggtatgatgc 2700
821 attctcaata tcacattatg cggtactttt gtttattat tccccatttg gtttgcataa 2760
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824 tattctgata attggatcat cacggatatac atttatgaaa ctgaagggttc cctcggtc 2940
825 aggttaatttt ccgcaatggc agaagtaaaa caggaaggca aagtcttctg tatcgtctc 3000
826 gtggcatgtt atctcagttt cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
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828 tggaaacatga cacttgtatc aaagataact agcaaaaacaa aactaaccctt tttctgaatt 3180
829 tcatattattt aggagttagtc gtgcctttaa aaaatttggt ttaagaaacc gaaaaacttag 3240
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832 actactgaag actaagataa tactgttttgc tggaaacactg cttgtatgt tctctgtact 3420
833 actgcaatata tggactctccg ctacttttgc tggattatgaa attgatctct tataggtacc 3480
834 ctatcattca ctctcttgc gcaagaatttgc gctcgacactt aaagttaaaca taacaatggc 3540
835 tccccaggtt ctcttttgc gttcctcacc ttatataatgat caaactttaa gtgtactttt 3600
836 ctgttatgtt gttgatttac ctccaaatttgc ttctttctaa aaatcatataa tctctgtact 3660
837 cctcaagaac ttgttataat ctaaacgaga ttctcattgg gaaaataaaa caacagccag 3720
838 aacacgatgg aagcgcacgtt catgtggaaac taaatgttgc tcatgagcat gggtcagaca 3780
839 tcatagctaa catgacaaaaa gcaccaaggg ttaagtacat aacctttat gaagactctg 3840
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843 <210> SEQ ID NO: 12

844 <211> LENGTH: 709

845 <212> TYPE: cDNA

846 <213> ORGANISM: Lv

848 <400> SEQUENCE: 12

849 ctggggccaa aagttaacat aacaaggaca ccacatgtcg agcatgtatc tcagatgtac 60

file:///C:/CRF4/Outhold/VsrI937779A.htm

11/18/05

RAW SEQUENCE LISTING DATE: 11/18/2005
PATENT APPLICATION: US/09/937,779A TIME: 10:08:48

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852	caggcgttgc	ggagcttgat	aaagcaaatc	acaggaacat	tgtcagatct	ccagcttga	240
853	tgcgggagct	gtggcttgag	atgtggcatg	atattcatcc	tgataaaaag	tccaagtttg	300
854	ttacaaaagg	tggtgtctga	tcctcaactat	tttcttctat	aatgtttga	gtttgtattt	360
855	acattgtaaag	tattgcaaca	aaaagcaaag	cgtgggcctc	tgagggatga	ggactgctat	420
856	tgggattacg	ggaaagctcg	atgtgcattgg	gctgaacatt	gtgaatacag	gttagaatat	480
857	tcaaattata	ttttgcaaaa	tattctcttt	ttgtgtatTT	aggccacctt	tccccggtca	540
858	caacgatgca	gatatgtatt	cggggatgtt	cacctggac	agagttgcag	attgaagagt	600
859	tctacatctc	acatcctgtc	acactatgtg	tgatatttaa	gaaactttgt	ttggcggAAC	660
860	aacaagtttgc	cacaacatt	tgaagaagaa	agcggaaatga	ttcagagag		709

2123 <210> SEQ ID NO: 23
2124 <211> LENGTH: 2312

, same error

E--> 2125 <212> TYPE: genomic DNA
2126 <213> ORGANISM: *Schizosaccharomyces pombe*

2128 <400> SEQUENCE: 23
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2131 acacaatctg tttcaaataa atcaagaaaa tctaaattt gaaaaagatt gaattttata 180
2132 tggcgctta ttttggaat atgcgtgct tttttttcg ctgttgaga cgacaatgct 240
2133 gtttcgacc ctgctacgtt agataaattt gggatatgc taggctctc agacttgtt 300
2134 gatgacatta aaggatattt atcttataat gtgttaagg atgcacctt tactacggac 360
2135 aaggcctcgc agtctcttag cgaaaatgaa gttcaagttt gcttgatat gtacaatgag 420
2136 ggatatcgaa gtgaccatcc ttttattatg gttcctgggtt ttatcagctc aggattagaa 480
2137 agtttgtcgt ttaataattt ctcgatttct tacttttagga aacgtctttt gggtagctgg 540
2138 tctatgctga aggcaatgtt ctttgcacaa caatgtggc ttgaacattt aatgcttgat 600
2139 aaaaaaaccg gcttggatcc gaagggatt aagctggag cagetcaggg gtttgaagca 660
2140 gctgattttt ttatcacggg ctattggatt tggagtaaag taattgaaaa ctttgcgtca 720
2141 atgggttatg agcctaataa catgttaagt gtttcttacg atggcgggtt atcatatgca 780
2142 aatttagagg aacgtataaa atattttca aagttaaaaa ttgttatttga gtacagcaac 840
2143 attgtacata agaaaaaggt agtgttattt ttcactcca tgggttcaca gtttacgtac 900
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2147 ggtgaaatga aagatacagg tattgtattt acattaaaca tggtaatatt taattttgc 1140
2148 taaccgtttt aagctcaattt gaatcgtttt tcggctatg ggttaagcaat aaattgttga 1200
2149 gatttggttac taatttactg tttagtttgg aaaaattttt ttcccgttct gaggtatatt 1260
2150 caaaaataca aatgtgtctt acttttcttca acttttataa gagagccatg atgggtcgca 1320
2151 ctatgggagg agtttattttt atgcttccat aaggaggcga tggtaatattt taattttgc 1380
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2158 ttgcgttac ggggtcgaa aaccaacttga gagaggttatttataacta ataattccgtt 1800
2159 gggcaacccgtt gtcatttgcattt cctcggtttaa tggtaatggaa aagttgaaa atgtgagaga 1860
2160 atttatgtttt caaacatttttcaatgtt ttatttaggtt atgttgcgtt gatgtgttgc 1920
2161 tggaaacttta ccaatatttgc cccttgggtt qgtgtqcaat aaqtttqqc aaacaaaaaq 1980

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

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Output Set: N:\CRF4\11182005\I937779A.raw

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2163 ttagtctgaga ggaggaccc gctcgccaga acacgtcgat atacttggac attcagagct 2100
2164 aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aagggaaatta 2160
2165 tttaaaagt ttcatcaggc catggtgact cggtacccaa ccgttatata tcagatatcc 2220
2166 agtacggaca taagtttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
2167 atgagataaa tctcgataaa cctagaaatt aa 2312

2170 <210> SEQ ID NO: 24

2171 <211> LENGTH: 3685

> same Error

E--> 2172 <212> TYPE: GenomicDNA

2173 <213> ORGANISM: Arabidopsis thaliana

2175 <400> SEQUENCE: 24

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2177 gtgggtgcacg atgaggattc gaaaaagaaa ccacacgaat cttccaaatc ccaccataag 120
2178 aaatcgaacg gaggaggaa gtggtcgtgc atcgattttt gttgttgggtt cattgggtgt 180
2179 gtgtgtgtaa cctgggtgggt tcttctcttc ctttacaacg caatgcctgc gagctccct 240
2180 cagttatgtaa cggagcgaat cacgggtctt ttgcctgacc cggccgggtgt taagctaaa 300
2181 aaagaaggctc ttaaggcgaat acatctgtt gtcttcattc ctgggattgtt caccgggtggg 360
2182 ctgcagctt gggaggcaaa acatgcgtt gatgtttat ttagaaaacg tttgtgggt 420
2183 ggaactttt gtaagtctt caaaagggtga gctcaacaat tctcactttt cctttatatt 480
2184 gggatttggaa ttgatcttga tgagatcagc cactgttgc ttcttcaaca tcactcaa 540
2185 tttaattcca tggatgtctg tcttactttt tactttttt tttttttagt gtgaaacgct 600
2186 attttcttaa gagactattt ctgtatgtt aaggttaagcg ttcaaggac gtaattggct 660
2187 tggactattt ctgtttgatt gtttaacttta ggtatataaaa tagctgcctt ggaatttcaa 720
2188 gtcatcttat tgccaaatct gttgctagac atgcctttaga gtccgttcat aacaagttac 780
2189 ttcccttact gtcgttgcgt gtagattttt ctgttgcgt tagtataatga agtagtgttt 840
2190 tatgttttgt tggaaataga gaagttctaa ctacatctgtt gggaaagtgtt ttcaggctgt 900
2191 gatagaggac tggatgttttta ttattcaact atgtatatgt gtaattaaag ctatgttccctt 960
2192 tttgatctttt cagctcaatg tgcttttctt aatttttttcaattttcaaa agttcacat 1020
2193 cgagtttattt cacatgtttt gatatttgcgtt catcctcggtt ctgttattcca gctttgaact 1080
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2195 acgatcttca tcttcttctt tcggctcagt gttcatgtttt ttgctatgggtt agagatgggc 1200
2196 aatgttattt tttgatgttca cagttgtata gttgatagta tcttaactaa tcaattatct 1260
2197 ctttgatcttca ggcttctatg ttgggtggaa cacatgttac ttgacaatga aactgggtt 1320
2198 gatccagctg gtatttagt tcgagctgtt tcaggactcg tggctgctga ctactttgtt 1380
2199 cctggctact ttgtctggc agtgcgttattt gctaacccttgc cacatattgg atatgaagag 1440
2200 aaaaatatgtt acatggctgc atatgactgg cggcttgcgtt ttcaacac agagttctt 1500
2201 ttctcatctgt tctttcttattt attctgttcc atgttacgtt tctttcttca ttacttaagg 1560
2202 cttaaatatgtt ttcatgttca aattaaatagg tacgtgtatca gactctttagc cgtatgaaaa 1620
2203 gtaatataaga gttgatgttca ttatccaacg gtggaaaaaaa agcagttata gttccgcattt 1680
2204 ccatgggggtt tttgttattt tcatattttta tgaatgtgggt tgaggccacca gtcctctgg 1740
2205 gtggcgccccccatg tggccatgtt tgggtgtccaa agtattttaa ggcgggtatg aacattgggt 1800
2206 gaccatttttctt tgggtttccaa aaagcttttgc cagggtttt ctctgttca gcaaaaggatg 1860
2207 ttgcagttgc cagttatttga atatctgtt attcttttga tgatcagaac cttggctctg 1920
2208 gaactcaaaat ttatttctactt aaatatcaat tctaataaca ttgctatattt atcgtgtcaa 1980
2209 ctgacatgg ttgattttt ttgctgttca tgtaactgaa actcttttgc gatttagacaa 2040
2210 atgatgaattt gataatttctt acgcatttgcgtt ctgtgtatgac cagtttcttca gtttcgacga 2100
2211 taacattttt catactgtctt tttgggggc attgaattttt gctatggaaa gcgctggagc 2160
2212 ttccatgttca gcatttttca ccaatttagcg ttattctgtt tctttcaattt ttctgtata 2220
2213 tgcatctatg gtcttttattt tcttcttaat taaagactcg ttggatttagt tgctcttata 2280

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

2214 gtcacttggc tccttaat agaactttac tttcttcgaa aattgcagag cgattgcccc 2340
 2215 aggattctta gacaccgata tattttagact tcagaccttg cagcatgtaa tgagaatgac 2400
 2216 acgcacatgg gactcaacaa tgtctatgtt accgaaggga ggtgacacga tatggggcgg 2460
 2217 gcttgattgg tcacccggaga aaggccacac ctgttgtggg aaaaagcaaa agaacaacga 2520
 2218 aacttgggtt gaagcaggtg aaaacggagt ttccaagaaa agtcctgtta actatggaag 2580
 2219 gatgatatct ttgggaaag aagtagcaga ggctgcgcc a tctgagatta ataatattga 2640
 2220 ttttcgagta aggacatata aatcataata aaccttgc ttttgc ttttgc ttttgc 2700
 2221 atatctgtac attttatctg gtgaagggtg ctgtcaaagg tcagagtatc ccaaatcaca 2760
 2222 cctgtcgta cgtgtggaca gagtaccatg acatggaa tgctggatc aaagctatcg 2820
 2223 ctgagtataa ggcttacact gctggtaag ctatagatct actacattat gttgtcccta 2880
 2224 agatgatggc gctgggtgc gtcattctt ctatggaa tgctgtatc ttggatgaca 2940
 2225 ccaagtatca agatcccaa tactggtcaa atccgttataa gacaaagtaa gtgatttctt 3000
 2226 gattccaaact gtatccctcg tccgtatc ttatcgtct ttttgc ttttgc 3060
 2227 gatatggttt tcagctcaa gcttacaaag ctgtttctga gccttctca aaaaggctt 3120
 2228 ctcagtaata ttgagggtct aaagttgata catgtactc ttgcttataa atccctccgtt 3180
 2229 tgggttgc tgc ttttca gattaccgaa tgctccgtatc atggaaatct actcattata 3240
 2230 cggagtgggg ataccaacgg aacgagcata cgtatataa cttaaccagt ctcccgacag 3300
 2231 ttgcattcccc tttagatat tcacttctgc tcacgaggag gacgaagata gctgtctgaa 3360
 2232 agcaggagtt tacaatgtgg atggggatga aacagtaccc gtcctaagtccgggtacat 3420
 2233 gtgtgcaaaa gcgtggcgtg gcaagacaag attcaaccct tccggatca agacttat 3480
 2234 aagagaatac aatactctc cgccggctaa cctgttggaa gggcgcggga cgcagagtgg 3540
 2235 tgcccattttt gatatcatgg gaaacttgc tttgategaa gatatcatga gggttgcgc 3600
 2236 cggaggtaac gggctgtata taggacatga ccaggtccac tctggatcatat ttgaatggtc 3660
 2237 ggagcgtatt gacctgaagc tgc tgc 3685
 2240 <210> SEQ ID NO: 25
 2241 <211> LENGTH: 402 *same error*

E--> 2242 <212> TYPE: CDNA

2243 <213> ORGANISM: Arabidopsis thaliana

2245 <220> FEATURE:

2246 <221> NAME/KEY: CDS

2247 <222> LOCATION: (120)..(401)

2249 <400> SEQUENCE: 25

2250 agaaacagct ctttgc tccgactgtat ctaacaatcc ctaatctgtg ttctaaattc 60

2252 ctggacgaga tttgacaaag tccgtatagc ttaacccgtt ttaatttcaa gtgacagat 119

2254 atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167

2255 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro

2256 1 5 10 15

2258 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215

2259 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His

2260 20 25 30

W--> 2262 gaa tct tcc aaa tcc cac cat aag nna tcg aac gga gga ggg aag tgg 263

W--> 2263 Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Lys Trp

2264 35 40 45

2266 tcg tgc atc gat tct tgt tgg ttc att ggg tgt gtg tgt gta acc 311

2267 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr

2268 50 55 60

2270 tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359

2271 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro

2272 65 70 75 80

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RAW SEQUENCE LISTING
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DATE: 11/18/2005
TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

See page 17

W--> 2274 cag tat gta acg gag ccg aat cac ~~sng~~ tcc ttt gcc tta ccc g 402
 W--> 2275 Gln Tyr Val Thr Glu Pro Asn His Xaa Ser Phe Ala Leu Pro
 2276 85 90
 2279 <210> SEQ ID NO: 26
 2280 <211> LENGTH: 643
 E--> 2281 <212> TYPE: cDNA → Same Error
 2282 <213> ORGANISM: Zea mays
 2284 <220> FEATURE:
 2285 <221> NAME/KEY: CDS
 2286 <222> LOCATION: (1)..(402)
 2288 <400> SEQUENCE: 26
 2290 cg~~g~~ gag aaa ata gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
 2291 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 2292 1 5 10 15
 2294 gat gaa act gtt cca gtt ctt agt g~~c~~ ggc tac atg tgt g~~c~~ gaa aag gga 96
 2295 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 2296 20 25 30
 2298 tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
 2299 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 2300 35 40 45
 2302 aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
 2303 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 2304 50 55 60
 2306 acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
 2307 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 2308 65 70 75 80
 2310 gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
 2311 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 2312 85 90 95
 2314 ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
 2315 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 2316 100 105 110
 2318 ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
 2319 Leu Lys Leu
 2320 115
 2322 g~~c~~ ttc caa agt gtc ctg cctgagt~~g~~ca actctggatt ttgcttaat 432
 2324 attgtatattttcacgcttc attcgccct ttgtcaaatt tacatttgac aggacgccaa 492
 2326 tg~~c~~gatacga tg~~t~~ttgtaccg ctat~~t~~ttcag cattgtatat taaactgtac aggtgtaa~~g~~t 552
 W--> 2328 tgcatttgcc agctgaaatt gtgttagt~~g~~t tttctttacg atttaat~~a~~ aagtggccga 612
 W--> 2330 gc~~a~~gtgc~~ccc~~ a~~gg~~aaaaaaa aaaaaaaaaa a 643
 2333 <210> SEQ ID NO: 27
 2334 <211> LENGTH: 115
 2335 <212> TYPE: PRT
 2336 <213> ORGANISM: Zea mays
 E--> 2338 <400> SEQUENCE: 30 → 27
 2339 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 2340 1 5 10 15
 2341 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 2342 20 25 30

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

2343 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
2344 35 40 45
2345 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
2346 50 55 60
2347 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
2348 65 70 75 80
2349 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
2350 85 90 95
2351 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
2352 100 105 110

2353 Leu Lys Leu
2354 115

2357 <210> SEQ ID NO: 28

2358 <211> LENGTH: 516

E--> 2359 <212> TYPE: CDNA
2360 <213> ORGANISM: Neurospora crassa

2362 <400> SEQUENCE: 28

E--> 2363 ggtggcgaag acg~~an~~ggcg~~g~~ aagtggagg ctaacgagaa tga~~n~~ctcg~~g~~ agatggatct 60
E--> 2364 acc~~c~~tc~~a~~g~~a~~ gacacgacta c~~o~~nttgcacc cag~~c~~ctcaag g~~m~~taqngtt t~~o~~atggta 120
2365 ggaagccgac ggagcgagcc tacatctatc tggccc~~g~~ tcccgggac~~g~~ acaacgcac~~t~~ 180
E--> 2366 tttagat~~g~~ac gatcgata~~c~~g actttgact~~n~~ agggcacat tgaccac~~g~~gt gtgattttgg 240
2367 gcgaaggcga tggcacagt~~g~~ aac~~c~~ttat~~g~~a gtttgggta cctgtgcaat aagg~~g~~tgga 300
2368 aaatgaagag atacaatct~~c~~ g~~c~~gggctcaa aaataacc~~g~~t ggtcgagat~~g~~ ccgc~~a~~tgaac 360
2369 cagaac~~c~~g~~t~~ caatccgaga ggagggccga atacggc~~g~~ga cttaaatat~~g~~ tagaaaaggt 420
2370 tgaaatttat gaagagtaat taaatac~~g~~gc acata~~g~~gtta ctcaatagta tgactaatta 480
2371 aaaaaaaaaatt tttttctaa aaaaaaaaaa aaaaaa 516

2374 <210> SEQ ID NO: 29

2375 <211> LENGTH: 1562

E--> 2376 <212> TYPE: genomic DNA
2377 <213> ORGANISM: Arabidopsis thaliana

2379 <400> SEQUENCE: 29

2380 ataaaaaaaa tatcttcaca ttattcgta gtcatagcga tactcg~~t~~tt ggtgacgat~~g~~ 60
2381 acctcgat~~g~~t gtcaagctgt gggtagcaac gtgtacc~~c~~tt tgattctgt~~g~~t tccaggaaac 120
2382 ggaggt~~a~~acc agctagaggt acggctggac agagaataca agccaagtag tgtctgg~~t~~gt 180
2383 agcagctgt tatatcc~~g~~t tcataagaag agtgg~~t~~ggat ggtttag~~g~~t atggttc~~g~~at 240
2384 gcagcag~~t~~gt tattgtctcc cttcaccagg tgcttc~~g~~cg atcgaat~~g~~at gtttactat 300
2385 gaccctgatt tggatgatta cccaaat~~g~~t cctgg~~t~~gtcc aaaccggg~~t~~ tcctcatttc 360
2386 gg~~t~~tcgacca aat~~c~~actt~~c~~t atac~~c~~tc~~g~~ac cctcg~~t~~ctcc gg~~t~~tagtact ttccaagata 420
2387 tattcattt~~g~~ ggacatttgc ataatgaaca aaat~~a~~gacat aaatttgggg gattattgtt 480
2388 atatcaat~~a~~at ccatttat~~g~~t gctagt~~c~~gg~~t~~aatgtgag~~t~~g ttat~~t~~ttat~~g~~t atat~~t~~taat~~g~~t 540
2389 tgagtgttat~~t~~ gtgattttcc attttaaat~~g~~a aag~~t~~agaaaa gttgtcg~~t~~tt aataat~~g~~tt 600
2390 ctatgtcat~~g~~ agaattataa ggacactat~~g~~ taaatgt~~g~~ac ttaataataa gg~~t~~ttg~~t~~ttt 660
2391 gcagagat~~g~~c cacat~~c~~ttac atggaacatt tgg~~t~~gaa~~g~~c tctagagaaaa aaatgcggg~~t~~ 720
2392 atgttaac~~g~~ca ccaaaccat~~c~~ ctaggag~~c~~t catatgattt caggtac~~g~~gc ctggctg~~c~~t 780
2393 cgggccaccc gtcccg~~t~~gt~~a~~ g~~c~~c~~t~~ca~~c~~act~~g~~t~~c~~ t~~c~~c~~t~~aca~~g~~aa ttgg~~t~~ggaaa 840
2394 aaactagc~~g~~ cgagaac~~g~~aa ggaaagcc~~g~~tgatact~~c~~c~~t~~ccccat~~g~~ac~~t~~ ctaggaggac 900
2395 tttt~~c~~gtct~~c~~c~~t~~ ccattt~~c~~c~~t~~ aacc~~g~~tac~~cc~~ cccctt~~c~~at~~g~~ g~~c~~g~~c~~g~~c~~ca~~g~~ tacat~~c~~aaac 960
2396 actttgt~~t~~gc~~c~~ actcg~~c~~ct~~g~~cc~~c~~catggg~~t~~g ggac~~g~~at~~c~~tc~~t~~ c~~t~~agat~~g~~aa~~g~~ acatttg~~c~~t 1020
2397 ctggcaacac~~a~~ actcg~~c~~gt~~c~~ cctttag~~t~~ta acc~~c~~tt~~t~~g~~c~~t ggtcagac~~g~~gg catcagagga 1080

RAW SEQUENCE LISTING DATE: 11/18/2005
PATENT APPLICATION: US/09/937,779A **TIME:** 10:08:48

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

2398 cctccgagag taaccaatgg ctacttccat ctaccaaagt gttcacgac agaactaaac 1140
2399 cgcttgctgt aactccccag gtaactaca cagttacga gatggatcggttttcgcag 1200
2400 acattggatt ctcacaagga gtgtgcctt acaagacaag agtgtgcct ttaacagagg 1260
2401 agctgatgac tccgggagtg ccagtcactt gcatatatgg gagaggagtt gatacaccgg 1320
2402 agttttgtat gtatggaaaa ggaggattcg ataagcaacc agagattaag tatggagatg 1380
2403 gagatgggac ggttaatttg gcgagcttag cagcttgaatgcata 1440
2404 tagagattga tggagttcg catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
2405 ttatgaagca gattcaattt attaattatg aattagccaa tgtaatgccgtcaatgaat 1560
2406 ga 1562
2407 2310 SEQ ID NO: 30

2409 <210> SEQ ID NO: 30
2410 <211> LENGTH: 3896

same error

E--> 2411 <212> TYPE: genomic DNA
2412 <213> ORGANISM: Arabidopsis thaliana
2414 <400> SEQUENCE: 30

2415 atggggcga attcgaaatc agtaacggct tccttcaccg tcatcgccgt tttttcttg 60
2416 atttgcggtg gccgaactgc ggtggaggat gagaccgagt ttacggcga ctactcgaaag 120
2417 ctatcggtta taatcattcc ggatttgcg tcgacgcgc tacgagcgtg gtcgatccct 180
2418 gactgtccat acactccgtt ggacttcaat cegctegacc tegtatggct agacaccaact 240
2419 aagggtccgtg atcttcattt ctttcgtcc ttattctgtc ggtcgagtca cttgttgatg 300
2420 aattccaagc gaaatatage aatgaagcat gtctcgctc tettattgtat tcgttcatta 360
2421 gtcAACAGTG acgcttctga atctgagttt agagtcatat aaaacagctg actcggcgag 420
2422 tgTTTCCCAt cgcttttgt tcgctaaatg tagcgaatg aatgtgtaat tagtctcg 480
2423 ttttattca actagatctg caagttttc agagtgtca atagtagtta gaaaatgtta 540
2424 ggtcatttttta cttgtgcatt gtgattctt tggttgttgc ttactgatcg acgtgtatgga 600
2425 tgTTTACAG cttcttctg ctgtcaactg ctggTTAAG tggatggtgc tagatccta 660
2426 taatcaaaca gaccatccc agtgtaagt acggcctgac agtggcttt cagccatcac 720
2427 agaattggat ccaggttaca taacaggtag tttcggattt ttctttctt tgagtttct 780
2428 tcaatttgat atcatttgt tggatataa tatggctaag ttcatTAATT tggtcaattt 840
2429 tcaggcctc tttctactgt ctggaaagag tggcttaagt ggtgtgtga gtttggata 900
2430 gaagcaaATG caattgtcgc tttccatac gattggagat tgcaccaac caaattggaa 960
2431 gagcgtgacc ttactttca caagctcaag ttgtccta tcaggctaatt gtctttatc 1020
2432 ttctttttt atgtaaagata agctaagagc tctggcgtc ttctttttg cagggtgacc 1080
2433 ttgaaACTG cttaaaact ccgtggcggc cttctatag tatttgccta ttcaatgggt 1140
2434 aataatgtct tcagataact tctggaatgg ctgaggctag aaattgcacc aaaacattat 1200
2435 ttgaagtggc ttgatcagca tatccatgct tatttcgtg tggTaccgg cctactatcc 1260
2436 ttaagttacc attttattt ttctctaatt gggggagtt tggatgtact tactggattg 1320
2437 agtcgatac ctgattttt gttgatTTT gagctctct tttggTTCT gttgaggcaa 1380
2438 tcaaATCTAC ttctctggt gtaacgttt gccttcgtt ttctgaggTg acctctgact 1440
2439 ttcttttagt tttaagttgt tgatatcaac caggctttat aactcaactgg attttccTTT 1500
2440 tggaaagtatt actttgtta attgaactgc tgtacgcgt atggatctg tagatcttga 1560
2441 agtgcTAGTT atcaaAGAAC atattgtggg tagtatacct gtacggcgc ttagctata 1620
2442 caaccaaacc acatgtacac tgatTTAGTT ttcaGATTAT tatggtagac ttAAAGTGA 1680
2443 gaagaaACTT tgactgaaat ctTTTATTt taatagcta tgatttggTTT attgaaatca 1740
2444 tttgacatAT tgacatgcgc ttctcatgtt tttgtggc aaggcttcag ggaactgctc 1800
2445 ggttggTGTc caattttttt ggtcggtcat tttggcttgc gcatTTCA aagaatgca 1860
2446 agggtgataa cacattctgg accatTTTTT ctgggggtgc tggaaagaaaa gataagcgcg 1920
2447 tataccactg tgatgaagag gaatatcaat caaaatattc tggctggccg acaaataatt 1980
2448 ttaacattga aattccTTCC actagcggtt agactctgtat tgcactgtg taacactaac 2040
2449 aaaatTTCA ccaaaqaaatgt tcactctcat attcgttcc tttgtatgtgt atccatcaat 2100

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

Input Set : N:\RJAVER\09937779.txt
Output Set: N:\CRP4\11182005\I937779A.raw

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:48

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

```

2504 <212> TYPE: PRT
2505 <213> ORGANISM: Conserved Sequence
E--> 2507 <400> SEQUENCE: 7 32
E--> 2508 Phe Xaa Lys Trp Val Glu Ala
2509 1 5
2517 2/58
2518 BASF-NAE 33 77 / 99 PCT 12.09.2000
E--> 2520 1
2522 1/58
2523 09/937,779 OA July 13, 2005
E--> 2524 Dalquist et al.

```

Invalid Response.
<213> can be either
Artificial, Unknown
or Genus Species.
Pls see Glens #
10 on Error
Summary Sheet.

pls delete

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:49

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:49

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

Error explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 2363
Seq#:7; N Pos. 601,627
Seq#:9; N Pos. 15,45,83,103,107,112,210
Seq#:25; N Pos. 240,385
Seq#:25; Xaa Pos. 41,89
Seq#:26; N Pos. 601,627
Seq#:28; N Pos. 15,45,83,103,107,112,210
Seq#:32; Xaa Pos. 2

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/937,779A

DATE: 11/18/2005
TIME: 10:08:49

Input Set : N:\RJAVED\09937779.txt
Output Set: N:\CRF4\11182005\I937779A.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:337 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:3
L:384 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:4
L:454 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:5
L:497 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:639 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:7
L:685 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:7
L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:552
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:612
L:718 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:9
L:722 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:723 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:725 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:737 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:10
L:772 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:11
L:845 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:12
L:2125 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:23
L:2172 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:24
L:2242 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:25
L:2262 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:25
L:2262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215
L:2263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:263
L:2274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:359
L:2275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:402
L:2281 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:26
L:2328 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26
L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:552
L:2330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:612
L:2338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:27 differs:30
L:2359 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:28
L:2363 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:2364 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:2366 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:2376 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:29
L:2411 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:30
L:2484 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:31
L:2507 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:7
L:2508 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:2520 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:2524 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2524 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:3
L:2524 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:10 SEQ:32